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Genomic Structure and Expression of Silkworm Glutathione S-Transferase

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Glutathione S-transferase (GST; EC 2.5.1.18) is a major family of detoxification enzymes found in most organisms. We describe here the cloning, expression and characterization of cDNAs encoding the GST1 and GST2 subunits from the silkworm, *Bombyx mori*. The GST1 and GST2 cDNA sequences comprised of 666 bp and 618 bp encoding 222 and 206 amino acid residues, respectively. Phylogenetic analysis confirmed the deduced protein sequences of *B. mori* GST being divided into two types, GST1 and GST2. The deduced amino acid sequences of the *B. mori* GST1 and GST2 cDNAs were closest to the *Manduca sexta* GST1 (58% protein sequence identity) and *Platynota idaeusalis* GST2 (63% protein sequence identity), respectively. To identify the genomic structure of the *B. mori* GST1 and GST2, furthermore, we designed a primer set based on the sequences of the *B mori* GST1 and GST2 cDNAs. The genomic structure of the *B. mori* GST1 and GST2 spans 4,371 bp and 3,470 bp and consisted of five exons and four exons, respectively. Northern blot analysis revealed that *B. mori* GST subunits showed midgut-specific expression. The cDNAs encoding the *B. mori* GST subunits were respectively expressed as approximately 25 kDa (GST1) and 23 kDa (GST2) polypeptides in baculovirus-infected insect cells. The mRNA expression of *B. mori* GST subunits in midgut was increased during the feeding of microorganisms such as *B. mori* nuclear polyhedrosis virus, *Bacillus thuringiensis*, and *Beauveria bassiana*, suggesting that the induction of *B. mori* GST subunits is involved in the direct detoxification as a mechanism of defense against microorganisms and chemicals.